

FIGURE 1A

1 GAATTGGCC CTGAGGCCA AGAATTGGC ACGAGCCCG GCGCCAGCG CAGGACAGC GCTGTCCAT CCCGGCGTC CACCCGCCAT GGGGCTTCC
CTTAAACCGG GAGCTCCGGT TCTTAAGCCG TGCTCCCGCG CCGGGTCGC GTCCGTTCG CGACACGTA GGGCCCGCAG GTGGCGGTA CCCGAGAGG
Me tGlyLeuSer
101 TGGAGCCCC GACCTCCACT GCTGATGATC CTGCTACTGG TGCTGTGCTT GTGGCTGCCA CTTGAGCAG GAAACTCCCT TGCCACAGAG AACAGTTTG
ACCTCGGGCG CTGAGAGTGA CGACTACTAG GACGATACCC ACGACAGCAA CACCGACCGT GAACCTTCGT CTTTGAAGGA ACGGTGTCT TTGTCCAAC
5 TrpSerProa rGProProle uLeuMetIle LeuLeuLeuV alLeuSerIle uTrpLeuPro LeuGlyAlaG LyAsnSerIle uAlaThrGlu AsnArgPheVal
201 TGAACAGCTG TACCCAGGCC AGAAGAAT GCGAGGCTAA TCCCGCTTGC AAGGCTGCC CTACAGACCT GGGCTCCCTG ACCTCCAGTT TAAGCAGCC
ACTGTGCGAC ATGGGTCCCG TCTTCTTTA CGCTCCGATT AGGGGGAACG TTCCGACGGA TGGTCTGGA CCCGAGGACG TGGAGGTCAA ATTGCTCCG
39 AsnSerCy sThrGlnAla ArgLysLysC ysgLubAlaAs nProAlaCys LysAlaAlaIat yrgLnhIshLe uGlySerCy s ThrSerSerL euSerArgPro
301 GCTGCCCCCTA GAGAGTCTG CCATGTCTGC AGACTGCCCTA GAGCAGCAG AACCACTCAG GAACACTCT CTGATAGACT GCAGGTCGA TCGCGGCATG
CGACGGGAAT CTCTTCAGAC GGTACAGACG TCTGACGGAT CTCCGTCTGC TTGTGAGTC CTGTGAGAG GACTATCTGA CGTCCACGGT AGCCCGCTAC
72 LeuProleu GluGluSerA IametSerAl aAspCysLeu GluAlaAlaG IuGlnLeuAr gAsnSerSer LeuIleAspC ySArgCysShi sArgArgMet
401 AAGCACCAG CTACCTGTCT GGACATTAT TGGACCGTTC ACCCTGCCCG AAGCTTGGT GACTACGAGT TGCATGTCTC ACCCTATGAA GACACAGTGA
TTGCTGTGTC GATGACAGA CCTGTAATA ACCTGGCAG TGGAGCGGC TTGGAACCA CTGACTTCA ACCTACAGAG TGGGATPACTT CTGTCTCCTC
105 LysHisGlnA IatThrCysLe uAspIleTy rTrpThrValh isProAlaAr gSerLeuGly AspTyrgLul euAspValse rProTyrgLul AspThrValThr
501 CCAGCAACC CTGCAAAATG AATCTTAGCA AGTTGAACAT GCTCAACCA GACTCGGACC TCTGCTTCAA ATTTGCTATG CTGTGTAATC TTGACGACAA
GGTGGTTTG GACTTTTAC TTAGAATCGT TCAACTTGTG CGAGTTTGT CTGAGCCTGG AGACGAGTT TAAACGATAC GACACATGAG AAGTCTGTT
139 SerLysPr oTrpLysMet AsnLeuSerL yslLeuAsnMe tLeuLysPro AspSerAspL euCysLeuL yspheAlaMet LeuCysThrL euHisAspLys
601 GTGTGACCGC CTGGCAAGG CCTACGGGGA GGCATGCTCA GGGATCCGCT GCCAGCGCA CCTGTGCTTA GCCCAGCTGC GCTCTTCTT TGAAGAAGCA
CACACTGGCG GACCGCTTCC GGATGCCCT CCGTAGAGT CCTTAGGCGA CGGTGCGGT GGAGACGGAT CGGGTCGACG CGAGGAAGAA ACTTCTCCGT
172 CysAspArg LeuArgLysA IatTyrgLyl uAlaCysSer GlyIleArgC ysgLnhArgHi sleuCysLeu AlaglnLeuA rgserPhePh eGluLysAla
701 GCAGAGTCC ACGCTCAGG TCTGTGCTG TGTCCCTGTG CACCAAGAGA TGGGGGCTGT GGGAGCGGC GCGGTAAAC CATCGCCCC AGTTGCGCCC
CGTCTCAGG TGGGAGTCC AGACGACGAC ACAGGACAC GTGTCTTCT ACGCCGACA CCCCTGCGCG CCGCATTTG GTAGCGGGG TCAACGCGCG
205 AlaGluSerh isAlaglnG lyleuLeuLeu CysProCysA IatProGluAs palagLysC yGlyLuhArgA rgsArgAsnTh rIleAlaPro SerCysAlaLeu
801 TGCTTCTGT AACCCCAAT TGCTGTGATC TGCGGAGCTT CTGCGGTGCG GACCTTTGT GCAGATCAG CCTGTAGGAC TTCCAGACCC ACTGTATCC
ACGAGAGACA TGGGGGTGA ACGGACGTAG ACGCTTGAÄ GACGACACG CTGGGAACA CGTGTAGTGC GGACTACTG AAGTGTGG TGAAGTAGG
239 ProSerVa lThrProAsn CysLeuAspL euArgSerPh eCysArgAla AspProLeuC ySArgSerAr gleuMetasp PheGlnThrh isCysHisPro
901 TATGACATC CTGAGGACTT GTGCAACTGA GCATGCCAGA TGTCTGCGGG CATACCTGGG GCTGATTGGG ACTGCCATGA CCCCAACTT CATCAGCAAG
ATACCTGTAG GAACCTGAA CACGTTGACT CGTCAAGTCT ACAGACGCCC GTATGACCC GACTTAACCC TGACGGTACT GGGGTTGAA GTACTCGTTC
272 MetaspIle LeuGlyThrC yAlaThrG l uGlnSerArg CysLeuArgA IatTyrlLeuG lyleuIleGly ThrAlaMet hTrProAsnPh eIleSerLys

1001 GTPCAACACTA CTGTTGCTT AAGCTGCACC TGCCGAGCA GCGGCAACT ACAGAGCAG TGTGAACAGC TGGAAAGGTC CTTCTCCAG AACCCCTGCC
CAGTTGTGAT GACAACGGAA TTGCACGTGG ACGGCTCCGT CGCCGTTGGA TGCTCTGCTC ACCTGTGTC GAAGAGGGTC TTGGGACGG
305 ValAsnThr hrValAlaIle uSerCysThr CysArgIlys exGlyAsnLe uGlnAspGlu CysGluGlnL euGluArgse rPheSerGln AsnProCysLeu
1101 TCGTGAGGC CATTCGAGCT AAGATGCGTT TCCACAGACA GCTCTCTCC CAGACTGGG CAGACTCTAC TTTTTCAGTG GTGACAGCAG AGAACAGCAA
AGCACTCCG GTAACCTCGA TTCTACGCAA AGGTGTCTGT CGAGAAGAG GTCTGACCC GTCTGAGATG AAAAAGTCAC CACGTGCTG TCTGTGCTT
339 ValGluAl aIleAlaAla LysMetArgP heHisArgI nLeuPheSer GlnAspTrpA IaAspSerTh rPheSerVal ValGlnGlnG InAsnSerAsn
1201 CCCTGCTCTG AGACTGCAGC CAGGCTACC CATTCCTTCT TTCTCCATCC TTCCCTTGAT TCTGCTGAG ACCCTCTGCT ACCTGGGCTT CCTCAGGGTC
GGGACGAGAC TCTGACCTCG GGTCCGATGG GTAAGAAAGA AAGAGTAGG AAGGAAGCTA AGACAGAGTC TGGGAGACCA TCGAACCCGAA GGAGTCCAG
372 ProIleLeu ArgLeuGlnP rArgLeuP rOileLeuSer PheSerIleL euProLeuI lLeuLeuGln ThrLeuTrp
1301 CTTTGTCTTC TCCACACACAC CCAGACTGAT TTGCAGGCTG TGTGTGGAGA GAACTCGCCA GCTGTGGAA GAAGACGAG CGTCTACAC AGCAACCCGG
GAAACAGAGAG AGGTGTGTG GGTCTGACTA AACGTCCGAC ACCACCTCTT CTTGAGCGGT CCGACACCTT CTCTGCGTC GCACGATGTG TCGTTGGGCC
1401 AACCAACCAAG GCATTCCGCA GCACATCCCG TCTGCTCCAG AAGAGTCTT AGAAGTAGG GCTGTGACCC TTCCGATCCT GAGCGGCTAG TTTCAAAAC
TTGTTGTGTC CGTAAGGCGT CGTGTAGGGC AGACGAGGTC TTCTCCAGAA TCTTCACTCC CGACACTGGG AAGCTTAGGA CTGCGCGATC AAAAGTTGG
1501 TCCCTTGCCC CTGCTTCCTT CTGGCTCAGG CTGCTCTCC TTAGGACTTT GTGGGTCCAG TTTTGCTTTC TGTTCGTATG GTGATTAAGC GCTCACCCTC
AGGGAACGGG GACGAAGGAA GACCGAGTCC GACGAGAGAG AATCCTGAAA CACCAGGTC AAAACGGAAG ACAAGACTAC CACTAATCCG CGAGTGGAGG
1601 AGCGCTTCTT CCTGTTTCCC AGGACCAACC AGAGGCTAAG GAATCAGTCA TTCCCTGTG CCTCTCCAG GAAGGCAAGC TAAAGGTTCY GAGGTGACTG
TCGCGAAGAA GGACAAAGGG TCTGTGTGG TCTCCGATTC CTTAGTCAGT AAGGACAAC GGAAGAGGTC CTTCCTGCCG ATTCCCAAGA CTCACACTGAC
1701 AGAAAAATGT TTCCTTGTG TGAAGGCTG GTGCTCCAGC CTCACGTC CTCTGAATGG AAGATAAAAA CCTGCTGGTG TCTTGACTGC TCTGCCAGGC
TCTTTTACA AAGAAACAC ACCTTCCGAC CACGAGCTG GAGGTGAGG GAGACTTACC TTCTATTTTT GGACGACCAC AGAACTGACG AGACGGTCCG
1801 AATCCTGAC ATTGGGCAT GAAGAGCTAA AGTCTTGGG TCTTGTTTAA CTCCTATTAC TGTCCCAAAA TTCCCTTAGT CCTTGGGTG ATGATTAAC
TTAGGACTTG TAAACCCGTA CTCTCGATT TCAGAAACCC AGAACAAATT GAGGATATG ACAGGGGTTT AAGGGATCA GGAACCCAG TACTAATTTG
1901 ATTTGACTT AAAAAAAAAA AAAAAAAAAA AAAAA
TAAACTGAA TTTTTTTTTT TTTTTTTTTT TTTT

FIGURE 18

hgFRA3 1 MVRP L N P R P L P P V V L M L L L L L P P S P L P L A A G D P L P T E S R L M N S C L Q A R R K
mGFRa3 1 - M G L S W S P R P P L L M I L L L V L S L W L P L G A G N S L A T E N R F V N S C T Q A R K K

hgFRA3 51 C Q A D P T C S A A Y H L D S C T S S I S T P L P S E E P S V P A D C L E A A Q Q L R N S S L I G
mGFRa3 48 C E A N P A C K A A Y O H L G S C T S S L S R P L P L E E S A M S A D C L E A A E Q L R N S S L I O

hgFRA3 101 C M C H R R M K N Q V A C L D I Y W T V H R A R S L G N Y E L D V S P Y E D T V T S K P W K M N L S
mGFRa3 98 C R C H R R M K H Q A T C L D I Y W T V H P A R S L G D Y E L D V S P Y E D T V T S K P W K M N L S

hgFRA3 151 K L N M L K P D S D L C L K F A M L C T L N D K C D R L R K A Y G E A C S G P H C Q R H V C L R Q L
mGFRa3 148 K L N M L K P D S D L C L K F A M L C T L H D K C D R L R K A Y G E A C S G I R C Q R H L C L A Q L

hgFRA3 201 L T F F E K A A E P H A Q G L L L C P C A P N D R G C G E R R R N T I A P N C A L P P V A P N C L E
mGFRa3 198 R S F F E K A A E S H A Q G L L L C P C A P E D A G C G E R R R N T I A P S C A L P S V T P N C L O

hgFRA3 251 L R R L C F S D P L C R S R L V D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M
mGFRa3 248 L R S F C R A D P L C R S R L M D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M

hgFRA3 301 T P N F V S H V N T S V A L S C T C R G S G N L Q E E C E M L E G F S H N P C L T E A I A A K M R
mGFRa3 298 T P N F I S K V N T T V A L S C T C R G S G N L Q D E C E Q L E R S F S Q N P C L V E A I A A K M R

hgFRA3 351 F H S Q L F S O D W P H P T F A V M A H O N E N P A V R P Q P W V P S L F S C T L P L I L L L S L W
mGFRa3 348 F H R Q L F S O D W A D S T F S V V Q O N S N P A L R L O P R L P I L S F S I L P L I L L O T L W

fig 4

FIGURE 3

48613 1 MVRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLOARRK
 48614 1 MVRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLOARRK

48613 51 CQADPTCSAAYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
 48614 51 CQADPTCSAAYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG

48613 101 CMCHRRMKNQVACLDIYWTVHRARSLGNYELOVSPYEOTVTSKPWKMNLS
 48614 101 CMCHRRMKNQVACLDIYWTVHRARSL.....

48613 151 KLNMLKP DSDLCLKFAMLC TLNDKCDRLR KAYGEACSGPHCORHVCLROL
 48614 127 DSDLCLKFAMLC TLNDKCDRLR KAYGEACSGPHCORHVCLROL

48613 201 LTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
 48614 170 LTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE

48613 251 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM
 48614 220 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM

48613 301 TPNFVSNVNTSVALSCTCRGSGNLOEECEMLEGFFSHNPCLTEAIAAKMR
 48614 270 TPNFVSNVNTSVALSCTCRGSGNLOEECEMLEGFFSHNPCLTEAIAAKMR

48613 351 FHSOLFSDQWPHPTFAVMAHQENPAVRPOPWVPSLFSCTLPLILLLSLW
 48614 320 FHSOLFSDQWPHPTFAVMAHQENPAVRPOPWVPSLFSCTLPLILLLSLW

fig 5

FIGURE 4

DNA48613.orf 1 A T G G T G C G C C C C C T G A A C C C G C G A C C G C T G C C G C C G T A G T C T G A T G T T
GDNF1a1.orf 1 A T G T T
GDNF1a2.orf 1 A T G A T C T T G G C A A A C G T C T T C T G C C T C T T C T T T C T

DNA48613.orf 51 G C T G C T G C T G C T G C C G C G T C G C C G C T G C C T C T C G C A G C C G G A G A C C C C C
GDNF1a1.orf 6 C C T G G C G A C C C T G T A C T T C G C G C T G C C G C T C T T G G A C T T G C T C C T G T C G G
GDNF1a2.orf 39 A G A C G A G A C C C T C C G C T C T T T G G C C A G C C C T T C C T C C C T G C A G G G C C C C G

DNA48613.orf 101 T T C C C A C A G A A A G C C G A C T C A T G A A C A G C T G T C T C C A G G C C A G A G G A A G
GDNF1a1.orf 56 C C G A A G T G A G G G G C G G A G A C C G C C T G G A T T G C G T G A A A G C C A G T G A T C A G
GDNF1a2.orf 89 A G C T C C A C G G C T G G C G C C C C C A G T G G A C T G T G T C C G G G C C A T G A G C T G

DNA48613.orf 151 T G C C A G G C T G A T C C C A C T G C A G T G C T G C C T A C C A C C A C T G G A T T C C T G
GDNF1a1.orf 106 T G C C T G A A G G A G C A G A G C T G C A G C A C A A G T A C C G C A G C T A A G G C A G T G
GDNF1a2.orf 139 T G T G C C G G C G A T C C A A C T G C A G C T C T C G C T A C C G C A C T C T G C G G C A G T G

DNA48613.orf 201 C A C C T C T A G C A T A A G C A C C C C A C T G C C C T . . . C A G A G G A G C C T T C G G T C C
GDNF1a1.orf 156 C G T G G C G G G C A A G G A G A C C A A C T T C A G C C T G G C A T C C G G C C T G G A G G C C A
GDNF1a2.orf 189 C C T G G C A G G C C G C G A C C G C A A C A C C A T G C T G G C C A

DNA48613.orf 248 C T G C T G A C T G C C T G G A G G C A G C A C A G C A A C T C A G G A A C A G C T C T C T G A T A
GDNF1a1.orf 206 A G G A T G A G T G C C G C A G C G C C A T G G A G G C C C T G A A G C A G A A G T C G C T C T A C
GDNF1a2.orf 224 A C A A G G A G T G C C A G G C G G C C T T G G A G G T C T T G C A G A G A G C C G C T G T A C

DNA48613.orf 298 G G C T G C A T G T G C C A C C G G C G C A T G A A G A A C C A G G T T G C C T G C T T G G A C A T
GDNF1a1.orf 256 A A C T G C C G C T G C A A G C G G G G T A T G A A G A A G G A G A A G A A C T G C C T G C G C A T
GDNF1a2.orf 274 G A C T G C C G C T G C A A G C G G G C A T G A A G A A G G A G C T G C A G T G T C T G C A G A T

DNA48613.orf 348 C T A T T G G A C C G T T C A C C G T G C C C G C A G C C T T G G T A A C T A T G A G C T G G A T G
GDNF1a1.orf 306 T T A C T G G A G C A T G T A C C A G A G C C T G C A G G G A A A T G A T C T G C T G G A G G A T T
GDNF1a2.orf 324 C T A C T G G A G C A T C A C C T G G G G C T G A C C G A G G G T G A G G A G T T C T A C G A A G

DNA48613.orf 398 T C T C C C C C T A T G A A G A C A C A G T G A C C A G C
GDNF1a1.orf 356 C C C C A T A T G A A C C A G T T A A C A G C A G A T T G T C A
GDNF1a2.orf 374 C C T C C C C C T A T G A G C C G G T G A C C T C C G C C T C T C G G A C A T C T T C A G G C T T

DNA48613.orf 427 A A A C C C T G G A A A A T G A A T C T C A G C A A A C T G A A C A T G C T C A A A C C A G A C T C
GDNF1a1.orf 388 G A T A T A T T C G G G T G G T C C A T T C A T A T C A G T G G A G C A C A T T C C C A A A G G
GDNF1a2.orf 424 G C T T C A A T C T T C T C A G G G A C A G G G C C A G A C C C G G T G G T C A G C G C C A A G A G

DNA48613.orf 477 A G A C C T C T G C C T C A A G T T T G C C A T G C T G T G T A C T C T C A A T G A C A A G T G T G
GDNF1a1.orf 438 G A A C A A C T G C C T G G A T G C A G C G A A G G C C T G C A A C C T C G A C G A C A T T T G C A
GDNF1a2.orf 474 C A A C C A T T G C C T G G A T G C T G C C A A G G C C T G C A A C C T G A A T G A C A A C T G C A

DNA48613.orf 527 A C C G G C T G C G C A A G G C C T A C G G G G A G G C G T G C T C C G G G C C C A C T G . . . C
GDNF1a1.orf 488 A G A A G T A C A G G T C G G C G T A C A T C A C C C C G T G C A C C A C A G C G T G T C . . . C
GDNF1a2.orf 524 A G A A G C T G C G C T C C T C C T A C A T C T C C A T C T G C A A C C G C G A G A T C T C G C C

DNA48613.orf 574 C A G C G C C A C G T C T G C C T C A G G C A G C T G C T C A C T T T C T T C G A G A A G G C C G C
GDNF1a1.orf 535 A A T G A T G T C T G C A A C C G C C G C A A G T G C C A C A A G G C C C T C C G G C A G T C T T
GDNF1a2.orf 574 A C G A G C G C T G C A A C C G C C G C A A G T G C C A C A A G G C C C T G C G C A G T T C T T

DNA48613.orf 624 C G A G C C C C A C G C G C A G G G C C T G C T A C T G T G C C C A T G T G C C C C A
GDNF1a1.orf 585 T G A C A A G G T C C C G G C A A G C A C A G C T A C G G A A T G C T C T T C T G C T C C T G C C
GDNF1a2.orf 624 C G A C C G G G T G C C C A G C G A G T A C A C C T A C C G C A T G C T C T T C T G C T C C T G C C

DNA48613.orf 668 A C G A C C G G G G C T G C G G G G A G C G C C G G C G A A C A C C A T C G C C C C A A C T G C
GDNF1a1.orf 635 G G G A C A T C G C C T G C A C A G A G C G G A G G C G A C A G A C C A T C G T G C C T G T G T G C
GDNF1a2.orf 674 A A G A C C A G G C G T G C G C T G A G C G C C G C G G C A A C C A T C T G C C C A G C T G C

FIGURE 5A

DNA48613.orf 718 G C G C T G C C . . . G C C T G T G G C C C C C A A C T G C C T G G A G C T G C G G C G C C T C T G
GDNFral.orf 685 T C C T A T G A A G A G A G G G A G A A G C C C A A C T G T T T G A A T T T G C A G G A C T C C T G
GDNFra2.orf 724 T C C T A T G A G G A C A A G G A G A A G C C C A A C T G C C T G G A C T G C G T G G C G T G T G

DNA48613.orf 765 C T T C T C C G A C C C G C T T T G C A G A T C A C G C C T G G T G G A T T T C C A G A C C A C T
GDNFral.orf 735 C A A G A C G A A T T A C A T C T G C A G A T C T G C C C T T G C G G A T T T T T T A C C A A C T
GDNFra2.orf 774 C C G G A C T G A C C A C C T G T G T C G G T C C G G C T G G C C G A C T T C C A T G C C A A T T

DNA48613.orf 815 G C C A T C C C A T G G A C A T C C T A G G A A C T T G T G C A A C A G A G C A G T C C A G A . . .
GDNFral.orf 785 G C C A G C C A G A G T C A A G G T C T G T C A G C A G C T G T C T A A A G G A A A A C T A C G C T
GDNFra2.orf 824 G T C G A G C C T C C T A C C A G A C G G T C A C C A G C T G C C T G C G G A C A A T T A C C A G

DNA48613.orf 862 . . . T G T C T A C G A G C A T A C C T G G G G C T G A T T G G G A C T G C C A T G A C C C C C A A
GDNFral.orf 835 G A C T G C C T C C T C G C C T A C T C G G G G C T T A T T G G C A C A G T C A T G A C C C C C A A
GDNFra2.orf 874 G C G T G T C T G G G C T C T A T G C T G G C A T G A T T G G G T T T G A C A T G A C A C C T A A

DNA48613.orf 909 C T T T G T C A G C A A T G T C A A C A C C A G T G T T G C C T T A A G C T G C A C C T
GDNFral.orf 885 C T A C A T A G A C T C C A G T A G C C T C A G T G T G C C C C A T G G T G T G A C T
GDNFra2.orf 924 C T A T G T G A C T C C A G C C C C A C T G C A T C G T G T G T C C C C C T G G T G C A G C T

DNA48613.orf 953 G C C G A G G C A G T G G C A A C C T G C A G G A G G A G T G T G A A A T G C T G G A A G G G T T C
GDNFral.orf 929 G C A G C A A C A G T G G G A A C G A C C T A G A A G A G T G C T T G A A A T T C T T G A A T T T C
GDNFra2.orf 974 G T C G T G G C A G C G G G A A C A T G G A G G A G A G T G T G A G A A G T T C T C A G G G A C

DNA48613.orf 1003 T T C T C C C A C A A C C C C T G C C T C A C G G A G G C C A T T G C A G C T A A G A T G C G T T T
GDNFral.orf 979 T T C A G G A C A A T A C A T G T C T T A A A A T G C A A T T C A A G C C T T T G G C A A T G G
GDNFra2.orf 1024 T T C A C C G A G A A C C C A T G C C T C C G G A A C G C C A T C A G G C C T T T G G C A A C G G

DNA48613.orf 1053 T C A C A G C C A A C T C T T C T C C C A G G A C T G G C C A C A C C C T A C C T T T G C T G T G A
GDNFral.orf 1029 C T C C G A T G T G A C C G T G T G G C A G C C A G C C T T C C C A G T A C A G A C C A C C A C T G
GDNFra2.orf 1074 C A C G G A C G T G A A C G T G T C C C A A A A G G C C C T C G T T C C A G G C C A C C A G G

DNA48613.orf 1103 T G G C A C A C C A G A A T G A A A C C C T G C T G T G A G G C C A C A G C C C T G G G T G C C C
GDNFral.orf 1079 C C A C T A C C A C C A C T G C C C T C C G G G T T A A G A A C A A A C C C C T G G G G C C A G C A
GDNFra2.orf 1124 C C C C T C G G G T G G A G A G A C G C C T T C T T T G C C A G A T G A C C T C A G T G A C A G T

DNA48613.orf 1153 T C T C T T T C T C C T G C A C G C T T C C C T T G A T T C T G C T C C T G A G C C T A T G G T A
GDNFral.orf 1129 G G G T C T G A G A A T G A A A T T C C C A C T C A T G T T T T G C C A C C G T G T G C A A A T T T
GDNFra2.orf 1174 A C C A G C T T G G G G A C C A G T G T C A T C A C C A C C T G C A C G T C T G T C C A G G A G C A

DNA48613.orf 1203 G
GDNFral.orf 1179 A C A G G C A C A G A A G C T G A A A T C C A A T G T G T C G G G C A A T A C A C A C T C T G T A
GDNFra2.orf 1224 G G G G C T G A A G G C C A A C A A C T C C A A A G A G T A A G C A T G T G C T T C A C A G A G C

GDNFral.orf 1229 T T T C C A A T G G T A A T T A T G A A A A G A A G G T C T C G G T G C T T C C A G C C A C A T A
GDNFra2.orf 1274 T C A C G A C A A A T A T C A T C C C A G G G A G T A A C A A G G T G A T C A A A C C T A A C T C A

GDNFral.orf 1279 A C C A C A A A A T C A A T G G C T G C T C C T C A A G C T G T G G T C T G A G C C C A C T G C T
GDNFra2.orf 1324 G G C C C A G C A G A G C C A G A C C G T C G G C T G C C T T G A C C G T G C T G T C T G T C C T

GDNFral.orf 1329 G G T C C T G T G G T A A C C G C T C T G T C C A C C C T A T T A T C T T T A A C A G A A A C A T
GDNFra2.orf 1374 G A T G C T G A A A C A G G C C T T G T A G

GDNFral.orf 1379 C A T A G

FIGURE 5B

DNA48613 1 MVRPLNPRPLPPVVLMLLLLPSPPLAAGDPLPTESRLMNSCLQARRK
GDNFRA1 1 MFLAT...LYFAL...PLLDLLLSA...EVSGGD...RL...DCVKASDQ
GDNFRA2 1 MILANVFCLFFFLDET LRS LASPS...SLOGPELHGWRPPV...DCVRANEL

DNA48613 51 CQADPTCSAAYVHHLDSCTSSSISTPLP...SEEPSVPADCLEAAQQLRNSSLI
GDNFRA1 56 CLKKEQSCSTKYRTLROCVAGKETNFSLASGLEAKDEC RSAMEALKOKSLY
GDNFRA2 47 CAAESNCSSRYRTLROCLAGRORN...TMLANKECQAALEVLQESPLY

DNA48613 100 GCMCHRRMKNQVACLQDIYWTVHRARSLGNYELDVSPYEDT VTSKPWKMNL
GDNFRA1 86 NCRCKRGMKKEKNCLRIYWSMYOSL...OGNDLLEDSPYEPVNSRLSDIFRV
GDNFRA2 92 DCRCKRGMKKEKLQCLQDIYWSIHLGLTEGE E FYEASPYEPVT SRLSDIFRL

DNA48613 150 SKL...NMLKPDSDLCLKFAMLCTLNDKCDRLRKAYGEAC S...
GDNFRA1 135 VPFIS...VEHI...PKGNCLDAAKACNLDDICKKYRSAYITPCTTSVS
GDNFRA2 142 ASIFSGTGADPVVSAKSNHCLDAAKACNLNDNCKKLRS SYISICNREIS P

DNA48613 188 GPHCQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAP
GDNFRA1 179 NDVCNRRKCHKALROFFDKVPAKHSYGM LFCSC...RDIAC TERRROTIVP
GDNFRA2 192 TERCNRRKCHKALROFFDRVPSEYTYRMLFCSC...ODQACAEERRROTILP

DNA48613 238 NCALPPVA...PNCLELRRLCFSDPLCRSRLVDFQTHCHP...MDILGTCA TEQ
GDNFRA1 227 VCSYEEREKPNCLNLQDSCKTNYICRSRLADFF TNGQPESRSVSSGLKEN
GDNFRA2 240 SCSYEDKEKPNCLDLRGVCR TDHLCRSRLADFHANC RASYQT VTS CPADN

DNA48613 286 -SRCLRAYLGLIGTAMTPNFVSNV...NTSVALSCTCRGSGNLOEECEMLE
GDNFRA1 277 YADCLLAYSGLIGTVMTPNYIDSS...SLSVAPWDCSN SGNLD EEC LKFL
GDNFRA2 290 YQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCS CRGSGNMEECEKFL

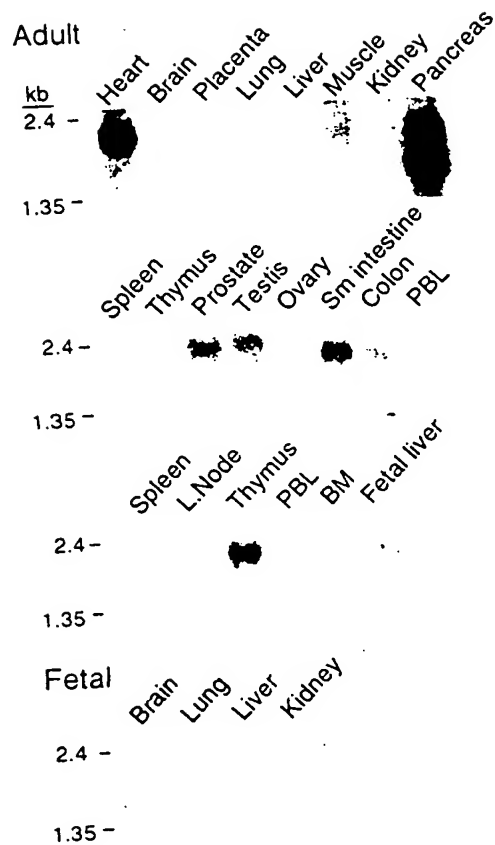
DNA48613 333 GFFSHNPCLTEAIAA...KMR FHSOLF S
GDNFRA1 325 NFFKONTCLXNAIOAFGNGSDVTWQPAFPVOTTTATTTTALRVKNKPLG
GDNFRA2 340 R D FTE NPCLRNAIOAFGNGT D VNVSPKGPSFOATOAPRVEKTPSLPDOLS

DNA48613 358 O...DWPHPTEFAVMAHQENPAVRPO...
GDNFRA1 375 PAGSENEIPTHVLP PCANLQAKLKS NVSGNTHLCISNGNYEKEGLGASS
GDNFRA2 390 DSTS...LGTSVITCTSVQEOGLKANN SKELSMCFT...ELTTNIIPGSN

DNA48613 381 - - - PWVPSLFSCTLP L L L L L L W - - - - -
GDNFRA1 425 HITTKSMAAPPSCGLSP L L V L V T A L S T L L S L T E T S
GDNFRA2 435 KVIK P NSGPSRRARPSAA L T V L S V L M L K Q A L - - - - -

FIGURE 6

protein alignment



NORTHERN BLOTS
FIGURE 7

GFR α 1

GFR α 2

GFR α 3



FIGURE 8

FIG. 9A

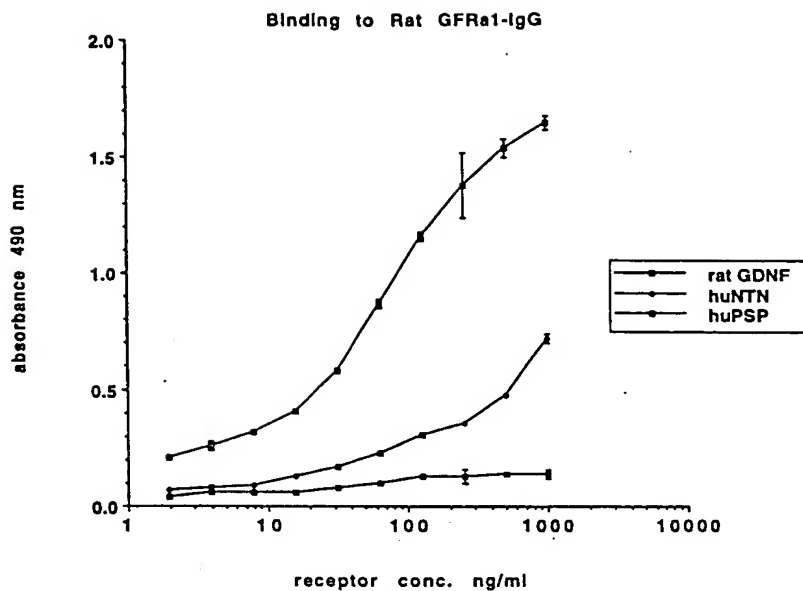


FIG. 9B

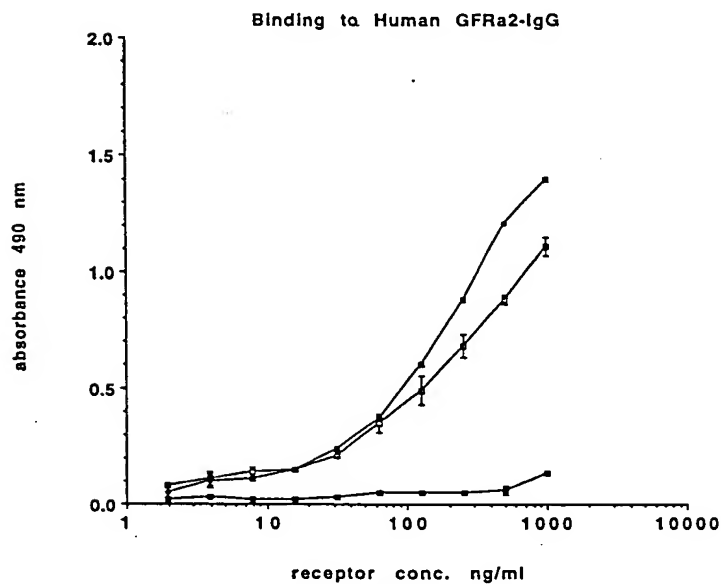
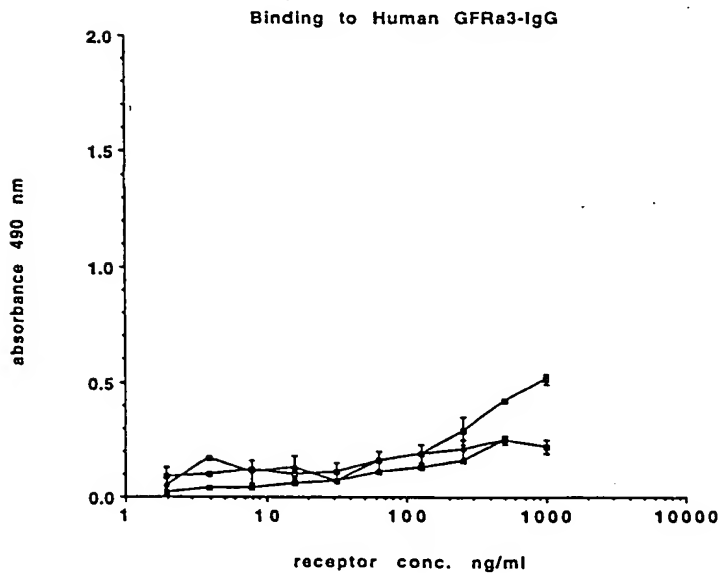


FIG. 9C



2
Proliferation of Ba/F3-GFRα₃-mpl cells in response to NTN and GDNF

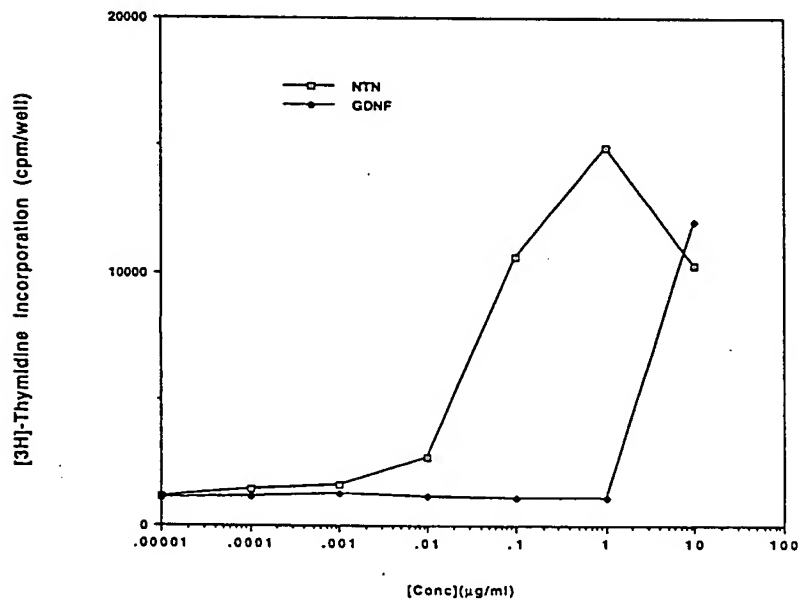


FIGURE 10

Phosphorylation of GFRa2-Rse in response to NTN

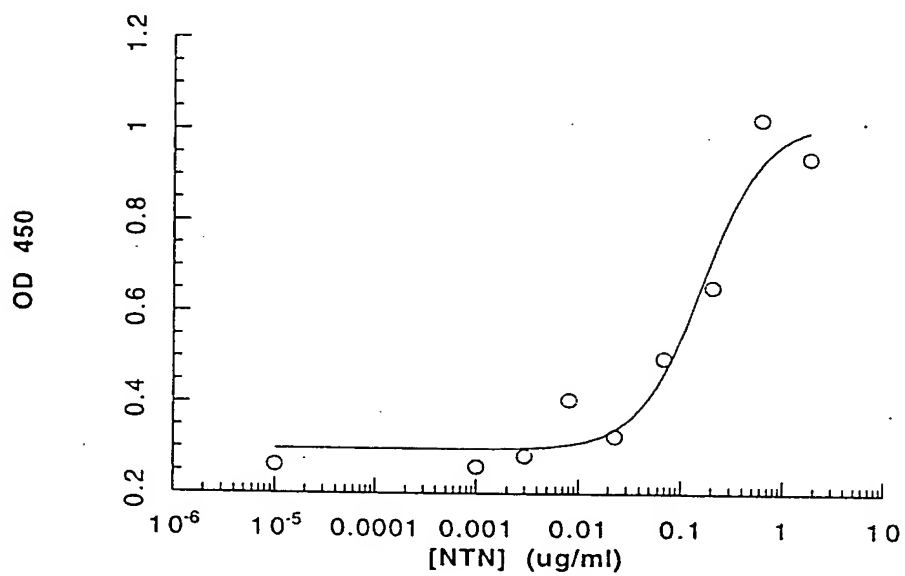


FIGURE 11

Stimulation of GFRa2 and GFRa3 by GDNF, NTN and PSN

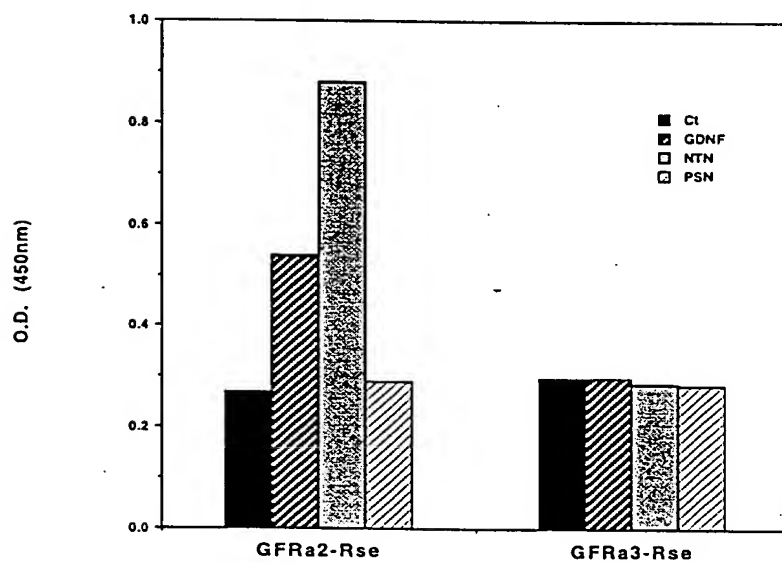


FIGURE 12

FIGURE 13

Agonistic activity of anti gD mAbs in gD-alpha2-rse KIRA

